

WHAT IS CLAIMED IS:

1. A method for determining the rate of biopolymer synthesis, wherein the biopolymer comprises a plurality of one or more monomer subunits, comprising:
  - 5 admixing a plurality of different monomer subunits, wherein at least one monomer subunit comprises a stable isotope probe, under conditions conducive to biopolymer synthesis;
  - incubating the monomer subunits for a time sufficient for at least two monomer subunits to incorporate into the biopolymer;
  - 10 isolating a sample of biopolymer from the admixture;
  - determining the abundance of monoisotopic and isotopomeric peaks for the sample of biopolymer;
  - calculating the difference between the abundance of monoisotopic and isotopomeric peaks determined for two separate time points; and
  - 15 dividing the calculated difference in the abundance of monoisotopic and isotopomeric peaks for the biopolymer by the time interval between time point.
2. The method of claim 1, wherein the biopolymer is an nucleic acid, a protein, a polypeptide, a peptide, a complex carbohydrate, or a lipid
3. The method of claim 2, wherein the nucleic acid is DNA,
  - 20 complementary DNA, ribosomal DNA, RNA, transfer RNA, messenger RNA, or nuclear RNA
4. The method of claim 1, wherein the stable isotope-labeled monomer is a deoxynucleic acid, an amino acid residue, a sugar, or a fatty acid.
5. The method of claim 1, wherein the biopolymer synthesis takes place
  - 25 in a cell, in an cell free system, or in an organism.
6. The method of claim 5, wherein the stable isotope-labeled monomer is added to a cell culture medium.

7. The method of claim 6, wherein the cell culture medium has been depleted of a monomer prior to admixing the stable isotope-labeled monomer.
8. The method of claim 1, wherein the biopolymer is separated by size, charge, hydrophilicity, specific affinity for a ligand, or differential solubility to form a group  
5 of separated parent polymers prior to determining the relative abundance of monoisotopic and isotopomeric peaks.
9. The method of claim 1, wherein a separated parent biopolymer is fragmented.
10. The method of claim 9, wherein the parent biopolymer is fragmented  
10 by an enzymatic means, a chemical means, or a physical stress.
11. The method of claim 10, wherein the enzymatic means is a protease, a restriction enzyme, or a lipase.
12. The method of claim 11, wherein the protease is trypsin, chymotrypsin, or papain.
13. The method of claim 10, wherein the chemical means is cyanogen  
15 bromide, or sodium borohydride.
14. The method of claim 10, wherein the fragmented parent biopolymer is separated by size, charge, hydrophilicity, or affinity.
15. The method of claim 1, wherein the biopolymer is detected by mass  
20 spectrometry, gas chromatography, gas chromatography/mass spectrometry, spectrophotometry, or ionization.
16. The method of claim 1, wherein the relative abundance of monoisotopic and isotopomeric peaks is determined by mass spectroscopy.
17. The method of claim 16, wherein the mass spectroscopy is matrix  
25 assisted desorption ionization mass spectroscopy, direct laser desorption ionization mass spectroscopy, electrospray ionization mass spectroscopy, secondary neutral mass spectroscopy, or secondary ion mass spectroscopy.

18. A method for determining the rate of degradation of a biopolymer, comprising;

a) enriching a first sample biopolymer pool with stable isotope-labeled monomer;

5 b) collecting an aliquot of the first sample of biopolymer;

c) measuring the relative abundance of monoisotopic and isotopomeric peaks in the first sample;

d) collecting a second aliquot of the first sample of biopolymer;

10 e) measuring the relative abundance of monoisotopic and isotopomeric peaks in the second aliquot;

f) calculating the difference between the relative abundance of monoisotopic and isotopomeric peaks measured for the second sample and the first sample;

15 g) dividing the calculated difference between the relative abundance of monoisotopic and isotopomeric peaks by the time duration between the first and second aliquot and therefrom determining the rate of polymer degradation.

19. The method of claim 18, wherein the biopolymer is a nucleic acid, a protein, a polypeptide, a peptide, a complex carbohydrate, or a lipid.

20. The method of claim 19, wherein the nucleic acid is a DNA, a complementary DNA, a ribosomal DNA, a RNA, a transfer RNA, a messenger RNA, or a nuclear RNA.

21. The method of claim 18, wherein the stable isotope-labeled monomer is a deoxynucleic acid, a ribonucleic acid, an amino acid, a sugar, or a fatty acid.

22. The method of claim 18, wherein the biopolymer degradation is measured in an organism, an isolated cell, or a cell free system.

25 23. The method of claim 18, wherein the biopolymer is separated to form a group of parent biopolymers.

24. The method of claim 23, wherein the parent biopolymer is fragmented.

25. The method of claim 24, wherein the biopolymer is fragmented by means of an enzyme, a chemical means, or physical stress.

5 26. The method of claim 25, wherein the enzyme is a protease, a nuclease, or a lipase.

27. The method of claim 25, wherein the chemical means is cyanogen bromide, or sodium borohydride.

10 28. The method of claim 25, wherein the protease is trypsin, chymotrypsin, or papain.

29. The method of claim 18, wherein the relative abundance of monoisotopic and isotopomeric peaks are corrected for the synthesis of new biopolymer.

15 30. The method of claim 29, wherein the relative abundance of newly synthesized biopolymer is determined in a second control sample which has been depleted of unlabeled monomer and incubated with stable isotope-labeled monomer for a time period sufficient for new biopolymer synthesis, the relative abundance of monoisotopic and isotopomeric peaks are determined at the time points used for the first sample; and the difference between the relative abundance of monoisotopic and isotopomeric peaks from the first and second sample is determined.